



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SUN, Yi
- (ii) TITLE OF INVENTION: SAG: Sensitive to Apoptosis Gene
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Warner-Lambert Company
 - (B) STREET: 2800 Plymouth Road
 - (C) CITY: Ann Arbor
 - (D) STATE: Michigan
 - (E) COUNTRY: USA
 - (F) ZIP: 48105
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/509,779
 - (B) FILING DATE: 03-29-2000
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: David R. Kurlandsky
 - (B) REGISTRATION NUMBER: 41,505
 - (C) REFERENCE/DOCKET NUMBER: 5650-01-DRK
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 734-622-7304
 - (B) TELEFAX: 734-622-1553

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 17..355
- (ix) FEATURE:
- (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 17..355

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION:1..1140

(D) OTHER INFORMATION:/note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

B.1. Cont

GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC	49
Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys	
1 5 10	
GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC	97
Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp	
15 20 25	
AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG	145
Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp	
30 35 40	
GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT	193
Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp	
45 50 55	
GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG	241
Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val	
60 65 70 75	
GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG	289
Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu	
80 85 90	
TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA	337
Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val	
95 100 105	
GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG	385
Val Gln Arg Ile Gly Lys	
110	
TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT	445
GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTTGG	505
GAAATTCTCT ACAATTAAGA TAATTTGTGA AAAATGGCCT TTCCTACCTC TGGTGTGTGT	565
GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC	625
CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA	685
AAAATAGATA AACGAATGTT ACAGTAACAA ATAAATGCA TTGAAAAGCC GACTCCTCCT	745
AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG	805
AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG	865
GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA	925

AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG 985
TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAATGGC TTACTAGTAT AACACTGAAG 1045
TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC 1105
TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG 1140

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His
1 5 10 15
Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:1..754

(D) OTHER INFORMATION:/note= "Human SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG 389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTCAGATT TGTCAGTTTT 509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749

TTAAA

754

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Fi
Cont

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1				5					10					15	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp
		35					40					45			
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys
	50					55					60				
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys
65				70					75					80	
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn
				85					90					95	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
		100						105					110		
Lys															

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide P1 downstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTTTTT TTTTTTTR

18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide: P2
upstream primer"

B1 Cont
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCTTNNNN NNN

13

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGGATCCCC ATGGCCGACG TGAGG

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGGGATCCTC ATTTGCCGAT TCTTTG

26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide P.01"

B1 Cont
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TATGGCTAGC ATGGCCGACG TGGAGG

26

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln	Asn	Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..270

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC

48

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG ATG CCT GTC TTA GAT GTC AAG CTG 192
 Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
 50 55 60

AAA ACA AAC AAG AGG ACT GTG TTG TGG TCT GGG GAG AAT GTA ATC ATT 240
 Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
 65 70 75 80

CCT TCC ACA ACT GCT GCA TGT CCC TGT GGG TGAAACAGAA CAATCGCTGC 290
 Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
 85 90

CCTCTCTGCC AGCAGGACTG GGTGGTCCAA AGAATCGGCA AATGAGAGTG GTTAGAAGGC 350

TTCTTAGCGC AGTTGTTTCTAG AGCCCTGGTG GATCTTGTA TCCAGTGCCC TACAAAGGCT 410

AGAACACTAC AGGGGATGAA TTCTTCAAAT AGGAGCCGAT GGATCTGTGG TCTTTGGACT 470

CATCAAAGCC TTGGTTAGCA TTTGTCTAGTT TTATCTTCAG AAATTCTCTG TGATTAAGAA 530

GATAATTTAT TAAAGGTGGT CCTTCCTACC TCTGTGGTGT GTGTCGCGCA CACAGCTTAG 590

AAGTGCTATA AAAAAGGAAA GAGCTCCAAA TTGAATCACC TTATAATTTA CCCATTTCTA 650

TACAACAGGC AGTGAAGCA GTTTCGAGAC TTTTTCGATG CTTATGGTTG ATCAGTTAAA 710

AAAGAATGTT ACAGTAACAA ATAAAGTGCA GTTTAAA 747

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
50 55 60

Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
65 70 75 80

Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
85 90

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..291

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTG GTC TGG GGA GAA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys	
50 55 60	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	240
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
65 70 75 80	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	288
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
85 90 95	

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA 341
 Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 401
 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 461
 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 521
 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 581
 GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 641
 TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 701
 TTAAA 706

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys
 50 55 60

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 65 70 75 80

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 85 90 95

Lys

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide hSAG. M1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCATCTGCA GGGTCCAG

18

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02L"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCTCAT TTGCCGATTC TTTGGAC

27

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide
SAGKanMX4-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTGCGAC

58

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX
4-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ACCTCGGTAT GATTTAAATG TTTACGGGCA ATTCATTTTT ATCGATGAAT TCGAGCTCG 59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Bel
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTCTCCAGTG GCAGAGAAC 19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATTTAAA TGTTTACGGG C 21

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG AGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	

35	40	45	
ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT			192
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys			
50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT			240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC			288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC			336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG			389
Lys			
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG			449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT			509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC			569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT			629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT			689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT			749
TTAAA			754

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20	30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35	45
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	

50		55		60
Gln Ala Glu Asn Lys	Gln Glu Asp Cys Val	Val Val Trp Gly Glu Cys		
65	70	75	80	
Asn His Ser Phe His	Asn Cys Cys Met Ser	Leu Trp Val Lys Gln Asn		
	85	90	95	
Asn Arg Cys Pro Leu	Cys Gln Gln Asp Trp	Val Val Gln Arg Ile Gly		
	100	105	110	

Lys

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288

Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
				85					90					95		
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
			100					105					110			
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTTCAGAG	CCCTGGTGGA											389
Lys																
TCTTGTAAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC											569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749
TTAAA																754

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1				5					10					15		
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
			20					25					30			
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	
			35				40					45				
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Ser	Leu	Arg	Cys	
			50			55					60					
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	
	65				70					75					80	
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	
				85				90						95		
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	
			100					105					110			

Lys

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..339

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA AGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Ser	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG	389
Lys	

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	1	5	10	15
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	20	25	30	
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	35	40	45	
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	50	55	60	
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Ser	65	70	75	80
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	85	90	95	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	100	105	110	
Lys																			

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT AAA TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTCAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749

TTAAA

754

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTCAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC AGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60
 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80
 Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn
 85 90 95
 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110
 Lys

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	

AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC AGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	

100

105

110

Lys

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192
 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60

CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240
 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80

AAT AAA TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC 288
 Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95

AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC 336
 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA 389
 Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	1	5	10	15
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	20	25	30	
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp	35	40	45	
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys	50	55	60	
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys	65	70	75	80
Asn	Lys	Ser	Phe	Lys	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn	85	90	95	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly	100	105	110	
Lys																			

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA AGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC AGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1             5             10             15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
      20             25             30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
      35             40             45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
      50             55             60
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys
      65             70             75             80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
      85             90             95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
      100            105            110
Lys
```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1             5             10             15
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
```

20	25	30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT			144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp			
35	40	45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA AGT			192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser			
50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT			240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys			
65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC			288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn			
85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC			336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA			389
Lys			
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG			449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT			509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC			569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT			629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT			689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT			749
TTAAA			754

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1				5					10					15	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45
 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser
 50 55 60
 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80
 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95
 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110
 Lys

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240

Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys		
65					70					75					80		
AAT	CAT	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC	288	
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
				85					90					95			
AAT	CGC	AGC	CCT	CTC	AGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC	336	
Asn	Arg	Ser	Pro	Leu	Ser	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly		
			100					105					110				
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTCAGAG	CCCTGGTGGA											389	
Lys																	
TCTTGTAAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG											449	
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT											509	
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC											569	
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT											629	
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT											689	
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT											749	
TTAAA																754	

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His		
1				5					10					15			
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu		
			20					25					30				
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp		
			35				40					45					
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys		
			50			55				60							
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys		
65				70					75						80		
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
				85				90						95			

Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..339

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG AGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA 389
Lys

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509

ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569

TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749

TTAAA 754

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys